IN THE SPECIFICATION:

Please insert the following Brief Description of the Drawings at page 9 of the specification, between lines 15 and 16.

-- BRIEF DESCRIPTION OF THE DRAWINGS

FIG. 1 shows the binding of ^{125}I-labeled Bt2 toxins to *M. sexta* brush border membrane vesicles as a function of the concentration of competitor.

FIG. 2 shows the binding of ^{125}I-labeled Bt3 toxins to *M. sexta* brush border membrane vesicles as a function of the concentration of competitor.

FIG. 3 shows the binding of ^{125}I-labeled Bt73 toxins to *M. sexta* brush border membrane vesicles as a function of the concentration of competitor.

FIG. 4 shows the binding of ^{125}I-labeled Bt2 toxins to *H. virescens* brush border membrane vesicles as a function of the concentration of competitor.

FIG. 5 shows the binding of ^{125}I-labeled Bt3 toxins to *H. virescens* brush border membrane vesicles as a function of the concentration of competitor.

FIG. 6 shows the binding of ^{125}I-labeled Bt73 toxins to *H. virescens* brush border membrane vesicles as a function of the concentration of competitor.

FIG. 7 shows the binding of ^{125}I-labeled Bt2 toxins to *P. brassicae* brush border membrane vesicles.

FIG. 8 shows the binding of ^{125}I-labeled Bt14 toxins to *P. brassicae* brush border membrane vesicles.

FIG. 9 shows the binding of ^{125}I-labeled Bt2 toxins to *M. sexta* brush border membrane vesicles.

FIG. 10 shows the binding of ^{125}I-labeled Bt15 toxins to *M. sexta* brush border membrane vesicles.

FIG. 11 shows the binding of ^{125}I-labeled Bt2 toxins to *M. sexta* brush border membrane vesicles

FIG. 12 shows the binding of ^{125}I-labeled Bt18 toxins to *M. sexta* brush border membrane vesicles.

FIG. 13 shows the nucleotide sequence and deduced amino acid sequence of the open reading frame of the bt4 gene, isolated from HD-68.

FIG. 14 shows the nucleotide sequence and deduced amino acid sequence of the open reading frame of the bt15 gene, isolated from HD-110.

FIGS. 15A-15C schematically show (a) the construction of pVE29; (b) the construction of pVE35; and (c) the construction of pTHW88.

FIGS. 16A-16E schematically show (a) the construction of pHW44; (b) the construction of pHW67; (c) the construction of pHW71; (d) the construction of pTHW94; and (e) restriction map of the pTHW94 vector.

FIG. 17 schematically shows the construction of a hybrid bt2-bt gene with a C-terminal bt2 gene fragment (bt860) encoding the toxic core of the Bt2 protoxin in frame with a C-terminal truncated bt14 gene fragment encoding the toxic core of the Bt14 protoxin. - -

Please replace the paragraph beginning on Page 26, line 15 and ending on Page 26, line 30 with the following:

bt4

gene: A genomic library was prepared from total DNA of strain *B. thuringiensis aizawai* HD-68. Using the 1.1 kb internal HindIII fragment of the *bt2* gene as a probe, a gene designated *bt4* was isolated. Characterization of this gene revealed an open reading frame of 3495 bp which encodes a protoxin of 132 kDa and a trypsin activated toxin fragment of 60 kDa. This (insect controlling protein) gene differs

from previously identified genes and was also found in several other strains of subspecies *aizawai* and *entomocidus* including HD-110. FIG. 13 shows the nucleotide sequence and deduced amino acid sequence of the open reading frame ("ORF") of the bt4 gene extending from nucleotide 264 to nucleotide 3761 (SEQ ID NO: 5).

Please replace the paragraph beginning on Page 27, line 9 and ending on Page 28, line 2 with the following:

The second gene was called "*bt15*". FIG. 14 shows the nucleotide sequence and deduced amino acid sequence of the ORF of the *bt15* gene, isolated from HD-110, extending from nucleotide 234 to nucleotide 3803 (SEQ ID NO: 5). The Shine and Dalgarno sequence, preceding the initiation codon is underlined. This gene has an open reading frame of 3567 bp which encodes a protoxin of 135 kDa and a 63 kDa toxin fragment. A similar gene has been described by Honee et al. 1988, isolated from *B. thuringiensis entomocidus* 60.5. The *bt15* gene differs from the published sequence at three positions: an Ala codon (GCA) is present instead of an Arg codon (CGA) at position 925 and a consecution of a Thr-His codon (ACGCAT) is present instead of a Thr-Asp codon (ACCGAT) at position 1400. (The numbers of the positions are according to Honnee et al., 1988). Another similar gene has been described in EP 0295156, isolated from *B. thuringiensis aizawai* 7-29 and *entomocidus* 6-01. The *bt15* gene is different from this published nucleotide sequence at three different places: 1) a Glu codon (GAA) instead of an Ala codon (GCA) at(position. 700; 2) the sequence (SEQ ID NO:1) TGG, CCA, GCG,

CCA instead of (SEQ ID NO:2) TGC, CAG, CGC, CAC, CAT at position 1456 and 3) an Arg codon (CGT) instead of an Ala codon (GCG) at position 2654. (The numbers of the positions are according to EP 0295156).